

0460
03/13/01

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#2

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/780,532

DATE: 03/08/2001
 TIME: 11:41:54

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\03082001\I780532.raw

3 <110> APPLICANT: Wood, Clive
 4 Chaudhary, Divya
 5 Long, Andrew
 7 <120> TITLE OF INVENTION: TRADE MOLECULES, AND USES RELATED THERETO
 9 <130> FILE REFERENCE: GNN-012CP
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/780,532
 C--> 12 <141> CURRENT FILING DATE: 2001-02-09
 14 <150> PRIOR APPLICATION NUMBER: 60/181,922
 15 <151> PRIOR FILING DATE: 2000-02-11
 17 <150> PRIOR APPLICATION NUMBER: 60/182,148
 18 <151> PRIOR FILING DATE: 2000-02-14
 20 <160> NUMBER OF SEQ ID NOS: 10
 22 <170> SOFTWARE: PatentIn Ver. 2.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1660
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <220> FEATURE:
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 36 1 5 10 15
 38 tta gta tta cta ggc tat ttg tca tgt aaa gtg act tgt gaa tca gga 96
 39 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Ser Gly
 40 20 25 30
 42 gac tgt aga cag caa gaa ttc agg gat cgg tct gga aac tgt gtt ccc 144
 43 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
 44 35 40 45
 46 tgc aac cag tgt ggg cca ggc atg gag ttg tct aag gaa tgt ggc ttc 192
 47 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
 48 50 55 60
 50 ggc tat ggg gag gat gca cag tgt gtg acg tgc cgg ctg cac agg ttc 240
 51 Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
 52 65 70 75 80
 54 aag gag gac tgg ggc ttc cag aaa tgc aag ccc tgt ctg gac tgc gca 288
 55 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala
 56 85 90 95
 58 gtg gtg aac cgc ttt cag aag gca aat tgt tca gcc acc agt gat gcc 336
 59 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala
 60 100 105 110
 62 atc tgc ggg gac tgc ttg cca gga ttt tat agg aag acg aaa ctt gtc 384
 63 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
 64 115 120 125
 66 ggc ttt caa gac atg gag tgt gtg cct tgt gga gac cct cct cct cct 432
 67 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro

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68      130      135      140
70 tac gaa ccg cac tgt gcc agc aag gtc aac ctc gtg aag atc gcg tcc 480
71 Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser
72 145      150      155      160
74 acg gcc tcc agc cca cgg gac acg gcg ctg gct gcc gtt atc tgc agc 528
75 Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
76      165      170      175
78 gct ctg gcc acc gtc ctg ctg gcc ctg ctc atc ctc tgt gtc atc tat 576
79 Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
80      180      185      190
82 tgt aag aga cag ttt atg gag aag aaa ccc agc tgg tct ctg cgg tca 624
83 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser
84      195      200      205
86 cag gac att cag tac aac ggc tct gag ctg tcg tgt ttt gac aga cct 672
87 Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Phe Asp Arg Pro
88      210      215      220
90 cag ctc cac gaa tat gcc cac aga gcc tgc tgc cag tgc cgc cgt gac 720
91 Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp
92 225      230      235      240
94 tca gtg cag acc tgc ggg ccg gtg cgc ttg ctc cca tcc atg tgc tgt 768
95 Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys
96      245      250      255
98 gag gag gcc tgc agc ccc aac ccg gcg act ctt ggt tgt ggg gtg cat 816
99 Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His
100      260      265      270
102 tct gca gcc agt ctt cag gca aga aac gca ggc cca gcc ggg gag atg 864
103 Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met
104      275      280      285
106 gtg ccg act ttc ttc gga tcc ctc acg cag tcc atc tgt ggc gag ttt 912
107 Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe
108      290      295      300
110 tca gat gcc tgg cct ctg atg cag aat ccc atg ggt ggt gac aac atc 960
111 Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile
112 305      310      315      320
114 tct ttt tgt gac tct tat cct gaa ctc act gga gaa gac att cat tct 1008
115 Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser
116      325      330      335
118 ctc aat cca gaa ctt gaa agc tca acg tct ttg gat tca aat agc agt 1056
119 Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser
120      340      345      350
122 caa gat ttg gtt ggt ggg gct gtt cca gtc cag tct cat tct gaa aac 1104
123 Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn
124      355      360      365
126 ttt aca gca gct act gat tta tct aga tat aac aac aca ctg gta gaa 1152
127 Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu
128      370      375      380
130 tca gca tca act cag gat gca cta act atg aga agc cag cta gat cag 1200
131 Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln
132 385      390      395      400

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134 gag agt ggc gct atc atc cac cca gcc act cag acg tcc ctc cag gaa 1248
135 Glu Ser Gly Ala Ile Ile His Pro Ala Thr Gln Thr Ser Leu Gln Glu
136          405          410          415
138 gct' taaagaacct gcttctttct gcagtagaag cgtgtgctgg aacccaaaga 1301
139 Ala
141 gtactccttt gttaggctta tggactgagc agtctggacc ttgcatggct tctggggcaa 1361
143 aaatgaatct gaaccaaact gacggcattt gaagcctttc agccagttgc ttctgagcca 1421
145 gaccagctgt aagctgaaac ctcaatgaat aacaagaaaa gactccaggc cgactcatga 1481
147 tactctgcat ttttcctaca tgagaagctt ctctgccaca aaagtgactt caaagacgga 1541
149 tgggttgagc tggcagccta tgagattgtg gacatataac aagaaacaga aatgccctca 1601
151 tgcttatttt catggtgatt gtggttttac aagactgaag acccagagta tactttttc 1660
154 <210> SEQ ID NO: 2
155 <211> LENGTH: 417
156 <212> TYPE: PRT
157 <213> ORGANISM: Homo sapiens
159 <400> SEQUENCE: 2
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163 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Ser Gly
164 20 25 30
166 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
167 35 40 45
169 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
170 50 55 60
172 Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
173 65 70 75 80
175 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala
176 85 90 95
178 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala
179 100 105 110
181 Ile Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
182 115 120 125
184 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
185 130 135 140
187 Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser
188 145 150 155 160
190 Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
191 165 170 175
193 Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
194 180 185 190
196 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser
197 195 200 205
199 Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Phe Asp Arg Pro
200 210 215 220
202 Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp
203 225 230 235 240
205 Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys
206 245 250 255
208 Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His

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209          260          265          270
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212          275          280          285
214 Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe
215          290          295          300
217 Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile
218 305          310          315          320
220 Ser Phe Cys Asp Ser Tyr Pro Glu Leu Thr Gly Glu Asp Ile His Ser
221          325          330          335
223 Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser
224          340          345          350
226 Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn
227          355          360          365
229 Phe Thr Ala Ala Thr Asp Leu Ser Arg Tyr Asn Asn Thr Leu Val Glu
230          370          375          380
232 Ser Ala Ser Thr Gln Asp Ala Leu Thr Met Arg Ser Gln Leu Asp Gln
233 385          390          395          400
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254 1          5          10          15
256 tta gta tta cta ggc tat ttg tca tgt aaa gtg act tgt gaa aca gga 96
257 Leu Val Leu Leu Gly Tyr Leu Ser Cys Lys Val Thr Cys Glu Thr Gly
258          20          25          30
260 gac tgt aga cag caa gaa ttc agg gat cgg tct gga aac tgt gtt ccc 144
261 Asp Cys Arg Gln Gln Glu Phe Arg Asp Arg Ser Gly Asn Cys Val Pro
262          35          40          45
264 tgc aac cag tgt ggg cca ggc atg gag ttg tct aag gaa tgt ggc ttc 192
265 Cys Asn Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
266          50          55          60
268 ggc tat ggg gag gat gca cag tgt gtg acg tgc cgg ctg cac agg ttc 240
269 Gly Tyr Gly Glu Asp Ala Gln Cys Val Thr Cys Arg Leu His Arg Phe
270 65          70          75          80
272 aag gag gac tgg ggc ttc cag aaa tgc aag ccc tgt ctg gac tgc gca 288
273 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Leu Asp Cys Ala
274          85          90          95
276 gtg gtg aac cgc ttt cag aag gca aat tgt tca gcc acc agt gat gcc 336
277 Val Val Asn Arg Phe Gln Lys Ala Asn Cys Ser Ala Thr Ser Asp Ala
278          100          105          110

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280 atc tgc ggc gac tgc ttg cca gga ttt tat agg aag acg aaa ctt gtc 384
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284 ggc ttt caa gac atg gag tgt gtg cct tgt gga gac cct cct cct cct 432
285 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
286      130      135      140
288 tac gaa ccg cac tgt gcc agc aag gtc aac ctc gtg aag atc gcg tcc 480
289 Tyr Glu Pro His Cys Ala Ser Lys Val Asn Leu Val Lys Ile Ala Ser
290 145      150      155      160
292 acg gcc tcc agc cca cgg gac acg gcg ctg gct gcc gtt atc tgc agc 528
293 Thr Ala Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
294      165      170      175
296 gct ctg gcc acc gtc ctg ctg gcc ctg ctc atc ctc tgt gtc atc tat 576
297 Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
298      180      185      190
300 tgt aag aga cag ttt atg gag aag aaa ccc agc tgg tct ctg cgg tca 624
301 Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Trp Ser Leu Arg Ser
302      195      200      205
304 cag gac att cag tac aac ggc tct gag ctg tcg tgt ctt gac aga cct 672
305 Gln Asp Ile Gln Tyr Asn Gly Ser Glu Leu Ser Cys Leu Asp Arg Pro
306      210      215      220
308 cag ctc cac gaa tat gcc cac aga gcc tgc tgc cag tgc cgc cgt gac 720
309 Gln Leu His Glu Tyr Ala His Arg Ala Cys Cys Gln Cys Arg Arg Asp
310 225      230      235      240
312 tca gtg cag acc tgc ggc ccg gtg cgc ttg ctc cca tcc atg tgc tgt 768
313 Ser Val Gln Thr Cys Gly Pro Val Arg Leu Leu Pro Ser Met Cys Cys
314      245      250      255
316 gag gag gcc tgc agc ccc aac ccg gcg act ctt ggt tgt ggg gtg cat 816
317 Glu Glu Ala Cys Ser Pro Asn Pro Ala Thr Leu Gly Cys Gly Val His
318      260      265      270
320 tct gca gcc agt ctt cag gca aga aac gca ggc cca gcc ggg gag atg 864
321 Ser Ala Ala Ser Leu Gln Ala Arg Asn Ala Gly Pro Ala Gly Glu Met
322      275      280      285
324 gtg ccg act ttc ttc gga tcc ctc acg cag tcc atc tgt ggc gag ttt 912
325 Val Pro Thr Phe Phe Gly Ser Leu Thr Gln Ser Ile Cys Gly Glu Phe
326      290      295      300
328 tca gat gcc tgg cct ctg atg cag aat ccc atg ggt ggt gac aac atc 960
329 Ser Asp Ala Trp Pro Leu Met Gln Asn Pro Met Gly Gly Asp Asn Ile
330 305      310      315      320
332 tct ttt tgt gac tct tat cct gaa ctc gct gga gaa gac att cat tct 1008
333 Ser Phe Cys Asp Ser Tyr Pro Glu Leu Ala Gly Glu Asp Ile His Ser
334      325      330      335
336 ctc aat cca gaa ctt gaa agc tca acg tct ttg gat tca aat agc agt 1056
337 Leu Asn Pro Glu Leu Glu Ser Ser Thr Ser Leu Asp Ser Asn Ser Ser
338      340      345      350
340 caa gat ttg gtt ggt ggg gct gtt cca gtc cag tct cat tct gaa aac 1104
341 Gln Asp Leu Val Gly Gly Ala Val Pro Val Gln Ser His Ser Glu Asn
342      355      360      365
344 ttt aca gca gct act gat tta tct aga tat aac aac aca ctg gta gaa 1152

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date